



SEQUENCE LISTING

<110> LIN, EDWARD H.

WU, XIFENG

XIE, KEPING

<120> QUANTITATIVE RT-PCR TO AC133 TO DIAGNOSE CANCER AND
MONITOR ANGIOGENIC ACTIVITY IN A CELL SAMPLE

<130> UTSC:755US

<140> 10/618,102

<141> 2003-07-11

<150> 60/406,535

<151> 2002-08-28

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 1

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<210> 2

<211> 30

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<223> Description of Artificial Sequence: Synthetic
Primer

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<211> 3794
<212> DNA
<213> Homo sapiens

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1 5

tcc ctg ttg ctg ctg ggg ctg tgc ggg aac tcc ttt tca gga ggg cag 103
Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln
10 15 20

cct tca tcc aca gat gct cct aag gct tgg aat tat gaa ttg cct gca 151
Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala
25 30 35

aca aat tat gag acc caa gac tcc cat aaa gct gga ccc att ggc att 199
Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile
40 45 50

ctc ttt gaa cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat 247
Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp
55 60 65 70

ttc cca gaa gat act ttg aga aaa ttc tta cag aag gca tat gaa tcc 295
Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser
75 80 85

aaa att gat tat gac aag cca gaa act gta atc tta ggt cta aag att 343
Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile
90 95 100

gtc tac tat gaa gca ggg att att cta tgc tgt gtc ctg ggg ctg ctg 391
Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu
105 110 115

ttt att att ctg atg cct ctg gtg ggg tat ttc ttt tgt atg tgt cgt 439
Phe Ile Ile Leu Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg
120 125 130

tgc tgt aac aaa tgt ggt gga gaa atg cac cag cga cag aag gaa aat 487
Cys Cys Asn Lys Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn
135 140 145 150

ggg ccc ttc ctg agg aaa tgc ttt gca atc tcc ctg ttg gtg att tgt		535
Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys		
155	160	165
ata ata ata agc att ggc atc ttc tat ggt ttt gtg gca aat cac cag		583
Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln		
170	175	180
gta aga acc cg ^g atc aaa agg agt cg ^g aaa ctg gca gat agc aat tt ^c		631
Val Arg Thr Arg Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe		
185	190	195
aag gac ttg cga act ctc ttg aat gaa act cca gag caa atc aaa tat		679
Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr		
200	205	210
ata ttg gcc cag tac aac act acc aag gac aag gc ^g tt ^c aca gat ct ^g		727
Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp Lys Ala Phe Thr Asp Leu		
215	220	225
230		
aac agt atc aat tca gtg cta gga ggc gga att ctt gac cga ctg aga		775
Asn Ser Ile Asn Ser Val Leu Gly Gly Ile Leu Asp Arg Leu Arg		
235	240	245
ccc aac atc atc cct gtt ctt gat gag att aag tcc atg gca aca gc ^g		823
Pro Asn Ile Ile Pro Val Leu Asp Glu Ile Lys Ser Met Ala Thr Ala		
250	255	260
atc aag gag acc aaa gag gc ^g ttg gag aac atg aac agc acc ttg aag		871
Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys		
265	270	275
agc ttg cac caa caa agt aca cag ctt agc agc agt ctg acc agc gt ^g		919
Ser Leu His Gln Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val		
280	285	290
aaa act agc ctg cg ^g tca tct ctc aat gac cct ctg tgc ttg gtg cat		967
Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His		
295	300	305
310		
cca tca agt gaa acc tgc aac agc atc aga ttg tct cta agc cag ct ^g		1015
Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu		
315	320	325
aat agc aac cct gaa ctg agg cag ctt cca ccc gtg gat gca gaa ctt		1063
Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu		
330	335	340

gac aac gtt aat aac gtt ctt agg aca gat ttg gat ggc ctg gtc caa			1111
Asp Asn Val Asn Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln			
345	350	355	
cag ggc tat caa tcc ctt aat gat ata cct gac aga gta caa cgc caa			1159
Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln			
360	365	370	
acc acg act gtc gta gca ggt atc aaa agg gtc ttg aat tcc att ggt			1207
Thr Thr Thr Val Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly			
375	380	385	390
tca gat atc gac aat gta act cag cgt ctt cct att cag gat ata ctc			1255
Ser Asp Ile Asp Asn Val Thr Gln Arg Leu Pro Ile Gln Asp Ile Leu			
395	400	405	
tca gca ttc tct gtt tat gtt aat aac act gaa agt tac atc cac aga			1303
Ser Ala Phe Ser Val Tyr Val Asn Asn Thr Glu Ser Tyr Ile His Arg			
410	415	420	
aat tta cct aca ttg gaa gag tat gat tca tac tgg tgg ctg ggt ggc			1351
Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser Tyr Trp Trp Leu Gly Gly			
425	430	435	
ctg gtc atc tgc tct ctg ctg acc ctc atc gtg att ttt tac tac ctg			1399
Leu Val Ile Cys Ser Leu Leu Thr Leu Ile Val Ile Phe Tyr Tyr Leu			
440	445	450	
ggc tta ctg tgt ggc gtg tgc ggc tat gac agg cat gcc acc ccg acc			1447
Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp Arg His Ala Thr Pro Thr			
455	460	465	470
acc cga ggc tgt gtc tcc aac acc gga ggc gtc ttc ctc atg gtt gga			1495
Thr Arg Gly Cys Val Ser Asn Thr Gly Gly Val Phe Leu Met Val Gly			
475	480	485	
gtt gga tta agt ttc ctc ttt tgc tgg ata ttg atg atc att gtg gtt			1543
Val Gly Leu Ser Phe Leu Phe Cys Trp Ile Leu Met Ile Ile Val Val			
490	495	500	
ctt acc ttt gtc ttt ggt gca aat gtg gaa aaa ctg atc tgt gaa cct			1591
Leu Thr Phe Val Phe Gly Ala Asn Val Glu Lys Leu Ile Cys Glu Pro			
505	510	515	
tac acg agc aag gaa tta ttc cgg gtt ttg gat aca ccc tac tta cta			1639
Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu Asp Thr Pro Tyr Leu Leu			
520	525	530	

aat gaa gac tgg gaa tac tat ctc tct ggg aag cta ttt aat aaa tca			1687
Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly Lys Leu Phe Asn Lys Ser			
535	540	545	550
aaa atg aag ctc act ttt gaa caa gtt tac agt gac tgc aaa aaa aat			1735
Lys Met Lys Leu Thr Phe Glu Gln Val Tyr Ser Asp Cys Lys Lys Asn			
555	560	565	
aga ggc act tac ggc act ctt cac ctg cag aac agc ttc aat atc agt			1783
Arg Gly Thr Tyr Gly Thr Leu His Leu Gln Asn Ser Phe Asn Ile Ser			
570	575	580	
gaa cat ctc aac att aat gag cat act gga agc ata agc agt gaa ttg			1831
Glu His Leu Asn Ile Asn Glu His Thr Gly Ser Ile Ser Ser Glu Leu			
585	590	595	
gaa agt ctg aag gta aat ctt aat atc ttt ctg ttg ggt gca gca gga			1879
Glu Ser Leu Lys Val Asn Leu Asn Ile Phe Leu Leu Gly Ala Ala Gly			
600	605	610	
aga aaa aac ctt cag gat ttt gct gct tgt gga ata gac aga atg aat			1927
Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn			
615	620	625	630
tat gac agc tac ttg gct cag act ggt aaa tcc ccc gca gga gtg aat			1975
Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn			
635	640	645	
ctt tta tca ttt gca tat gat cta gaa gca aaa gca aac agt ttg ccc			2023
Leu Leu Ser Phe Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro			
650	655	660	
cca gga aat ttg agg aac tcc ctg aaa aga gat gca caa act att aaa			2071
Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys			
665	670	675	
aca att cac cag caa cga gtc ctt cct ata gaa caa tca ctg agc act			2119
Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr			
680	685	690	
cta tac caa agc gtc aag ata ctt caa cgc aca ggg aat gga ttg ttg			2167
Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu			
695	700	705	710
gag aga gta act agg att cta gct tct ctg gat ttt gct cag aac ttc			2215
Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe			
715	720	725	

atc aca aac aat act tcc tct gtt att att gag gaa act aag aag tat 2263
Ile Thr Asn Asn Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr
730 735 740

ggg aga aca ata ata gga tat ttt gaa cat tat ctg cag tgg atc gag 2311
Gly Arg Thr Ile Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu
745 750 755

ttc tct atc agt gag aaa gtg gca tcg tgc aaa cct gtg gcc acc gct 2359
Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala
760 765 770

cta gat act gct gtt gat gtc ttt ctg tgt agc tac att atc gac ccc 2407
Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro
775 780 785 790

ttg aat ttg ttt tgg ttt ggc ata gga aaa gct act gta ttt tta ctt 2455
Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu
795 800 805

ccg gct cta att ttt gcg gta aaa ctg gct aag tac tat cgt cga atg 2503
Pro Ala Leu Ile Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met
810 815 820

gat tcg gag gac gtg tac gat gat gtt gaa act ata ccc atg aaa aat 2551
Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn
825 830 835

atg gaa aat ggt aat aat ggt tat cat aaa gat cat gta tat ggt att 2599
Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile
840 845 850

cac aat cct gtt atg aca agc cca tca caa cat tga tagctgatgt 2645
His Asn Pro Val Met Thr Ser Pro Ser Gln His
855 860 865

tgaaaactgct tgagcatcag gatactcaaa gtggaaagga tcacagattt ttggtagttt 2705

ctgggtctac aaggactttc caaatccagg agcaacgcca gtggcaacgt agtgactcag 2765

gcgggcacca aggcaacggc accattggc tctggtagt gctttaagaa tgaacacaat 2825

cacgttatacg tccatggtcc atcactattc aaggatgact ccctcccttc ctgtctattt 2885

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atcagcaatg aagaactggc cgacaaaat ttaacgttga tgtaatggaa ttccagatgt 3725
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ggaacttgg 3794

<210> 4
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<212> PRT
<213> Homo sapiens

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Asn Tyr Glu Leu Pro Ala Thr Asn Tyr Glu Thr Gln Asp Ser His Lys
35 40 45
Ala Gly Pro Ile Gly Ile Leu Phe Glu Leu Val His Ile Phe Leu Tyr
50 55 60
Val Val Gln Pro Arg Asp Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu
65 70 75 80
Gln Lys Ala Tyr Glu Ser Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val
85 90 95

Ile Leu Gly Leu Lys Ile Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys
100 105 110
Cys Val Leu Gly Leu Leu Phe Ile Ile Leu Met Pro Leu Val Gly Tyr
115 120 125
Phe Phe Cys Met Cys Arg Cys Cys Asn Lys Cys Gly Gly Glu Met His
130 135 140
Gln Arg Gln Lys Glu Asn Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile
145 150 155 160
Ser Leu Leu Val Ile Cys Ile Ile Ser Ile Gly Ile Phe Tyr Gly
165 170 175
Phe Val Ala Asn His Gln Val Arg Thr Arg Ile Lys Arg Ser Arg Lys
180 185 190
Leu Ala Asp Ser Asn Phe Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr
195 200 205
Pro Glu Gln Ile Lys Tyr Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp
210 215 220
Lys Ala Phe Thr Asp Leu Asn Ser Ile Asn Ser Val Leu Gly Gly Gly
225 230 235 240
Ile Leu Asp Arg Leu Arg Pro Asn Ile Ile Pro Val Leu Asp Glu Ile
245 250 255
Lys Ser Met Ala Thr Ala Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn
260 265 270
Met Asn Ser Thr Leu Lys Ser Leu His Gln Gln Ser Thr Gln Leu Ser
275 280 285
Ser Ser Leu Thr Ser Val Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp
290 295 300
Pro Leu Cys Leu Val His Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg
305 310 315 320
Leu Ser Leu Ser Gln Leu Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro
325 330 335
Pro Val Asp Ala Glu Leu Asp Asn Val Asn Asn Val Leu Arg Thr Asp
340 345 350
Leu Asp Gly Leu Val Gln Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro
355 360 365
Asp Arg Val Gln Arg Gln Thr Thr Thr Val Val Ala Gly Ile Lys Arg
370 375 380
Val Leu Asn Ser Ile Gly Ser Asp Ile Asp Asn Val Thr Gln Arg Leu
385 390 395 400
Pro Ile Gln Asp Ile Leu Ser Ala Phe Ser Val Tyr Val Asn Asn Thr
405 410 415
Glu Ser Tyr Ile His Arg Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser
420 425 430
Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys Ser Leu Leu Thr Leu Ile
435 440 445
Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp
450 455 460
Arg His Ala Thr Pro Thr Thr Arg Gly Cys Val Ser Asn Thr Gly Gly
465 470 475 480

Val Phe Leu Met Val Gly Val Gly Leu Ser Phe Leu Phe Cys Trp Ile
485 490 495
Leu Met Ile Ile Val Val Leu Thr Phe Val Phe Gly Ala Asn Val Glu
500 505 510
Lys Leu Ile Cys Glu Pro Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu
515 520 525
Asp Thr Pro Tyr Leu Leu Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly
530 535 540
Lys Leu Phe Asn Lys Ser Lys Met Lys Leu Thr Phe Glu Gln Val Tyr
545 550 555 560
Ser Asp Cys Lys Lys Asn Arg Gly Thr Tyr Gly Thr Leu His Leu Gln
565 570 575
Asn Ser Phe Asn Ile Ser Glu His Leu Asn Ile Asn Glu His Thr Gly
580 585 590
Ser Ile Ser Ser Glu Leu Glu Ser Leu Lys Val Asn Leu Asn Ile Phe
595 600 605
Leu Leu Gly Ala Ala Gly Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys
610 615 620
Gly Ile Asp Arg Met Asn Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys
625 630 635 640
Ser Pro Ala Gly Val Asn Leu Leu Ser Phe Ala Tyr Asp Leu Glu Ala
645 650 655
Lys Ala Asn Ser Leu Pro Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg
660 665 670
Asp Ala Gln Thr Ile Lys Thr Ile His Gln Gln Arg Val Leu Pro Ile
675 680 685
Glu Gln Ser Leu Ser Thr Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg
690 695 700
Thr Gly Asn Gly Leu Leu Glu Arg Val Thr Arg Ile Leu Ala Ser Leu
705 710 715 720
Asp Phe Ala Gln Asn Phe Ile Thr Asn Asn Thr Ser Ser Val Ile Ile
725 730 735
Glu Glu Thr Lys Lys Tyr Gly Arg Thr Ile Ile Gly Tyr Phe Glu His
740 745 750
Tyr Leu Gln Trp Ile Glu Phe Ser Ile Ser Glu Lys Val Ala Ser Cys
755 760 765
Lys Pro Val Ala Thr Ala Leu Asp Thr Ala Val Asp Val Phe Leu Cys
770 775 780
Ser Tyr Ile Ile Asp Pro Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys
785 790 795 800
Ala Thr Val Phe Leu Leu Pro Ala Leu Ile Phe Ala Val Lys Leu Ala
805 810 815
Lys Tyr Tyr Arg Arg Met Asp Ser Glu Asp Val Tyr Asp Asp Val Glu
820 825 830
Thr Ile Pro Met Lys Asn Met Glu Asn Gly Asn Asn Gly Tyr His Lys
835 840 845
Asp His Val Tyr Gly Ile His Asn Pro Val Met Thr Ser Pro Ser Gln
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His
865

<210> 5
<211> 20
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

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<210> 6
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Primer

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<210> 7
<211> 21
<212> DNA
<213> Artificial Sequence

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Primer

<400> 7
cttcaccacc atggagaagg c 21

<210> 8
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<212> DNA
<213> Artificial Sequence

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Primer

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<210> 9
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<213> Artificial Sequence

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Primer

<400> 9
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23

<210> 10
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<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 10
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<210> 11
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 11
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22

<210> 12
<211> 21
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 12
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21

<210> 13
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13
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<210> 14
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<212> DNA
<213> Artificial Sequence

<220>
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Primer

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28